

SEQUENCING LISTING

<110> KIM. Jin Woo

<120> Novel human cervical cancer 1 protooncogene and protein encoded therein

<130> PCA00211/KJW

<150> KR 1999-44811

<151> 1999-10-15

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<170> KOPATIN 1.5

<210> 1

<211> 2118

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(1088)

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<221> sig_peptide

<222> (9)..(83)

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<221> misc_feature

<222> (435)..(494)

<223> transmembrane domain

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ggc tcg gca gtc acc cct gga cat ttt gtc acc cgg agg ctg caa ctt 98
Gly Ser Ala Val Thr Pro Gly His Phe Val Thr Arg Arg Leu Gln Leu
15 20 25 30

ggt cgc tct ggc ctg gct tgg ggg gcc cct cgg tct tca aag ctt cac 146
Gly Arg Ser Gly Leu Ala Trp Gly Ala Pro Arg Ser Ser Lys Leu His
35 40 45

ctt tct cca aag gca gat gtg aag aac ttg atg tct tat gtg gta acc 194
Leu Ser Pro Lys Ala Asp Val Lys Asn Leu Met Ser Tyr Val Val Thr
50 55 60

aag aca aaa gcg att aat ggg aaa tac cat cgt ttc ttg ggt cgt cat 242
Lys Thr Lys Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His
65 70 75

ttc ccc cgc ttc tat atc ctg tac aca atc ttc atg aaa gga ttg cag 290
Phe Pro Arg Phe Tyr Ile Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln
80 85 90

atg tta tgg gct gat gcc aaa aag gct aga aga ata aag aca aat atg 338
Met Leu Trp Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met
95 100 105 110

tgg aag cac aat ata aag ttt cat caa ctt cca tac cgg gag atg gag 386
Trp Lys His Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu
115 120 125

cat ttg aga cag ttc cgc caa gac gtc acc aag tgt ctt ttc cta ggt	434
His Leu Arg Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly	
130 135 140	
att att tcc att cca cct ttt gcc aac tac ctg gtc ttc ttg cta atg	482
Ile Ile Ser Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met	
145 150 155	
tac ctg ttt ccc agg caa cta ctg atc agg cat ttc tgg acc cca aaa	530
Tyr Leu Phe Pro Arg Gln Leu Leu Ile Arg His Phe Trp Thr Pro Lys	
160 165 170	
caa caa act gat ttc tta gat atc tat cat gct ttc cgg aag cag tcc	578
Gln Gln Thr Asp Phe Leu Asp Ile Tyr His Ala Phe Arg Lys Gln Ser	
175 180 185 190	
cac cca gaa att att agt tat tta gaa aag gtc atc cct ctc att tct	626
His Pro Glu Ile Ile Ser Tyr Leu Glu Lys Val Ile Pro Leu Ile Ser	
195 200 205	
gat gca gga ctc cgg tgg cgt ctg aca gat ctg tgc acc aag ata cag	674
Asp Ala Gly Leu Arg Trp Arg Leu Thr Asp Leu Cys Thr Lys Ile Gln	
210 215 220	
cgt ggt acc cac cca gca ata cat gat atc ttg gct ctg aga gag tgt	722
Arg Gly Thr His Pro Ala Ile His Asp Ile Leu Ala Leu Arg Glu Cys	
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ttc tct aac cat cct ctg ggc atg aac caa ctc cag gct ttg cac gtg	770
Phe Ser Asn His Pro Leu Gly Met Asn Gln Leu Gln Ala Leu His Val	
240 245 250	

aaa gcc ttg agc cgg gcc atg ctt ctc aca tct tac ctg cct cct ccc 818
Lys Ala Leu Ser Arg Ala Met Leu Leu Thr Ser Tyr Leu Pro Pro Pro
255 260 265 270

ttg ttg aga cat cgt ttg aag act cat aca act gtg att cac caa ctg 866
Leu Leu Arg His Arg Leu Lys Thr His Thr Thr Val Ile His Gln Leu
275 280 285

gac aag gct ttg gca aag ctg ggg att ggc cag ctg act gct cag gaa 914
Asp Lys Ala Leu Ala Lys Leu Gly Ile Gly Gln Leu Thr Ala Gln Glu
290 295 300

gta aaa tcg gct tgt tat ctc cgt ggc ctg aat tct acg cat att ggt 962
Val Lys Ser Ala Cys Tyr Leu Arg Gly Leu Asn Ser Thr His Ile Gly
305 310 315

gaa gat agg tgt cga act tgg ctg gga gaa tgg ctg cag att tcc tgc 1010
Glu Asp Arg Cys Arg Thr Trp Leu Gly Glu Trp Leu Gln Ile Ser Cys
320 325 330

agc ctg aaa gaa gct gag ctg tct ctc ttg ctg cac aac gtg gtc ctg 1058
 Ser Leu Lys Glu Ala Glu Leu Ser Leu Leu Leu His Asn Val Val Leu
 335 340 345 350

ctc tcc acc aac tac ctt ggg aca agg cgc tg aatgaaccat ggagcgggatg 1110
Leu Ser Thr Asn Tyr Leu Gly Thr Arg Arg
355 360

gcattgtcct gcagtcgtat agtatagcag tgcaggaaca aacagcactt gccagcaaag 1170

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<211> 360

<212> PRT

<213> Homo sapiens

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Ala Val Thr Pro Gly His Phe Val Thr Arg Arg Leu Gln Leu Gly Arg
20 25 30

Ser Gly Leu Ala Trp Gly Ala Pro Arg Ser Ser Lys Leu His Leu Ser
35 40 45

Pro Lys Ala Asp Val Lys Asn Leu Met Ser Tyr Val Val Thr Lys Thr
50 55 60

Lys Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His Phe Pro
65 70 75 80

Arg Phe Tyr Ile Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln Met Leu
85 90 95

Trp Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met Trp Lys
100 105 110

His Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu His Leu
115 120 125

Arg Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly Ile Ile
130 135 140

Ser Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met Tyr Leu
145 150 155 160

Phe Pro Arg Gln Leu Leu Ile Arg His Phe Trp Thr Pro Lys Gln Gln
165 170 175

Thr Asp Phe Leu Asp Ile Tyr His Ala Phe Arg Lys Gln Ser His Pro
180 185 190

Glu Ile Ile Ser Tyr Leu Glu Lys Val Ile Pro Leu Ile Ser Asp Ala
195 200 205

Gly Leu Arg Trp Arg Leu Thr Asp Leu Cys Thr Lys Ile Gln Arg Gly
210 215 220

Thr His Pro Ala Ile His Asp Ile Leu Ala Leu Arg Glu Cys Phe Ser
225 230 235 240

Asn His Pro Leu Gly Met Asn Gln Leu Gln Ala Leu His Val Lys Ala
245 250 255

Leu Ser Arg Ala Met Leu Leu Thr Ser Tyr Leu Pro Pro Pro Leu Leu
260 265 270

Arg His Arg Leu Lys Thr His Thr Thr Val Ile His Gln Leu Asp Lys
275 280 285

Ala Leu Ala Lys Leu Gly Ile Gly Gln Leu Thr Ala Gln Glu Val Lys
290 295 300

Ser Ala Cys Tyr Leu Arg Gly Leu Asn Ser Thr His Ile Gly Glu Asp
305 310 315 320

Arg Cys Arg Thr Trp Leu Gly Glu Trp Leu Gln Ile Ser Cys Ser Leu
325 330 335

Lys Glu Ala Glu Leu Ser Leu Leu Leu His Asn Val Val Leu Leu Ser
340 345 350

Thr Asn Tyr Leu Gly Thr Arg Arg
355 360

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<223> anti-sense DNA

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<210> 4
<211> 18
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<220>
<223> sense DNA

<400> 4
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<210> 5
<211> 18

09/868474

9

<212> DNA
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<223> missense DNA

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<223> forward primer

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<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> reverse primer

<400> 7
gcttccggaa agcatgatag

20